

AMENDMENTS TO THE CLAIMS

1.– 13. (Cancelled)

14. (Currently Amended) A computer-implemented method of generating a local-global alignment score which indicates a global and a local similarity between a first protein structure and a second protein structure, the method comprising:

receiving a protein structure correspondence wherein a plurality of positions in the protein structure correspondence indicates a corresponding pair of residues in the first protein structure and the second protein structure;

determining a plurality of root mean square deviations corresponding to a plurality of sets of pairs of residues, wherein each set of pairs of residues comprises a plurality of pairs of residues that are contiguous in the protein structure correspondences and the plurality of root mean square deviations are determined using a plurality of specified threshold values;

selecting a longest contiguous segment corresponding to a set of pairs of residues of the plurality of pairs of residues based on the plurality of root mean square deviations

~~identifying a longest contiguous segment comprising a plurality of contiguous positions in the correspondence, wherein the root-mean-square deviation of a set of pairs of residues within the longest contiguous segment is less than a specified threshold value of the plurality of threshold values;~~

identifying a plurality of distance scores, wherein each distance score
corresponds to a number of pairs of residues in the
correspondence that are within a pre-defined distance of a
plurality of pre-defined distances
selecting identifying a global distance test value metric based on the
plurality of distance scores a number of pairs of residues in
the correspondence that are within a pre-determined distance
of each other;
generating the local-global alignment score based on the longest
contiguous segment and the global distance test value metric;
and
providing a result based on storing the local-global alignment score.

15. (Cancelled)

16. (Cancelled)

17. (Cancelled)

18. (Cancelled)

19. (New) The method of claim 14, further comprising:

receiving, at a server, a first set of co-ordinates associated with the first
protein structure from a client;

receiving, at the server, a second set of co-ordinates associated the second
protein structure; and

generating, at the server, the protein structure correspondence based on the
first set of co-ordinates and the second set of co-ordinates.

20. (New) The method of claim 14, further comprising:
- receiving a first set of co-ordinates associated with the first protein structure;
 - receiving a second set of co-ordinates associated the second protein structure;
 - and
 - generating the protein structure correspondence based on the first set of co-ordinates and the second set of co-ordinates.
21. (New) The method of claim 20, wherein providing a result based on the local-global alignment score further comprises:
- generating a second protein structure correspondence based on the local-global alignment score; and
 - providing the second protein structure correspondence.
22. (New) The method of claim 20, wherein providing the second protein structure correspondence comprises:
- modifying the set of co-ordinates specifying the first protein structure based on at last one of the global distance test value and the longest continuous segment; and
 - providing the modified set of co-ordinates.
23. (New) The method of claim 21, wherein providing the second protein structure correspondence comprises:
- displaying a graphical representation of at least one of the first protein structure or the second protein structure, wherein at least some of the

residues in the graphical representation are colored according to distance between the at last some of the residues and the corresponding residues in the second protein structure.

24. (New) The method of claim 23, wherein the graphical representation is a bar plot.

25. (New) The method of claim 23, wherein the graphical representation is a three-dimensional protein structure.